

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 26, 2002, 20:33:11 ; Search time 78 Seconds

(without alignments)  
2182.359 Million cell updates/sec

Title: US-09-840-795-18\_COPY\_78\_770

Perfect score: 693  
Sequence: 1 atggattgcgaagaataa.....agcagcagggcgctgaatg 693

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Issued Patents.NA.\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTCUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfileseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | length  | ID                | Description        |
|------------|-------|-------------|---------|-------------------|--------------------|
| 1          | 151.2 | 21.8        | 893     | US-09-286-529-8   | Sequence 8, Appli  |
| 2          | 132.8 | 19.2        | 623     | US-09-286-529-9   | Sequence 9, Appli  |
| 3          | 38.6  | 5.6         | 1347    | US-09-342-681C-16 | Sequence 16, Appli |
| 4          | 38.6  | 5.6         | 4235    | US-09-342-681C-18 | Sequence 18, Appli |
| 5          | 32    | 4.6         | 2242    | US-09-400-742-1   | Sequence 1, Appli  |
| 6          | 32    | 4.6         | 2242    | US-08-618-651A-1  | Sequence 1, Appli  |
| 7          | 32    | 4.6         | 2242    | US-09-215-252-1   | Sequence 1, Appli  |
| 8          | 31.8  | 4.6         | 3066    | US-08-142-439A-1  | Sequence 1, Appli  |
| 9          | 31.8  | 4.6         | 3066    | US-08-869-477-1   | Sequence 1, Appli  |
| 10         | 31    | 4.5         | 4315    | US-08-882-046-3   | Sequence 3, Appli  |
| 11         | 31    | 4.5         | 4464    | US-08-400-159-7   | Sequence 3, Appli  |
| 12         | 31    | 4.5         | 4483    | US-08-611-729A-7  | Sequence 7, Appli  |
| 13         | 31    | 4.5         | 50341   | US-08-247-901C-1  | Sequence 1, Appli  |
| 14         | 31    | 4.5         | 50341   | US-09-075-904-1   | Sequence 1, Appli  |
| 15         | 31    | 4.5         | 52297   | US-09-426-436-1   | Sequence 1, Appli  |
| 16         | 31    | 4.5         | 52297   | US-08-705-557-1   | Sequence 1, Appli  |
| 17         | 30.8  | 4.4         | 2055    | US-09-197-218-1   | Sequence 1, Appli  |
| 18         | 30.6  | 4.4         | 4403765 | US-09-103-840A-2  | Sequence 2, Appli  |
| 19         | 30.6  | 4.4         | 4411529 | US-09-103-840A-1  | Sequence 10, Appli |
| 20         | 30.4  | 4.4         | 1408    | US-08-222-124-10  | Sequence 10, Appli |
| 21         | 30.4  | 4.4         | 1408    | US-08-842-657A-10 | Sequence 10, Appli |
| 22         | 30.4  | 4.4         | 1414    | US-08-222-124-9   | Sequence 9, Appli  |
| 23         | 30.4  | 4.4         | 1414    | US-08-842-657A-9  | Sequence 9, Appli  |
| 24         | 30.4  | 4.4         | 9840    | US-09-534-638-1   | Sequence 1, Appli  |
| 25         | 30.4  | 4.4         | 15378   | US-08-785-420-1   | Sequence 1, Appli  |
| 26         | 30.2  | 4.4         | 1969    | US-08-966-318-4   | Sequence 4, Appli  |
| 27         | 30.2  | 4.4         | 1969    | US-09-216-619-4   | Sequence 4, Appli  |

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| 28 | 30.2 | 4.4 | 2522  | US-09-058-389A-1  | Sequence 1, Appli  |
| 29 | 30   | 4.3 | 7218  | US-08-232-463-14  | Sequence 14, Appli |
| 30 | 30   | 4.3 | 53526 | US-08-658-136-2   | Sequence 2, Appli  |
| 31 | 30   | 4.3 | 53577 | US-08-658-136-1   | Sequence 1, Appli  |
| 32 | 29.8 | 4.3 | 1050  | US-09-459-774-1   | Sequence 1, Appli  |
| 33 | 29.8 | 4.3 | 48974 | US-08-920-422-17  | Sequence 17, Appli |
| 34 | 29.6 | 4.3 | 981   | US-08-349-696-20  | Sequence 20, Appli |
| 35 | 29.6 | 4.3 | 981   | US-08-233-009-20  | Sequence 20, Appli |
| 36 | 29.6 | 4.3 | 981   | US-08-560-231-20  | Sequence 20, Appli |
| 37 | 29.6 | 4.3 | 981   | US-09-080-704A-20 | Sequence 20, Appli |
| 38 | 29.6 | 4.3 | 1343  | US-08-718-738-3   | Sequence 3, Appli  |
| 39 | 29.6 | 4.3 | 1343  | US-09-221-844-3   | Sequence 3, Appli  |
| 40 | 29.6 | 4.3 | 1995  | US-08-425-069-3   | Sequence 3, Appli  |
| 41 | 29.6 | 4.3 | 1995  | US-08-317-844B-3  | Sequence 3, Appli  |
| 42 | 29.6 | 4.3 | 2180  | US-07-918-314-3   | Sequence 3, Appli  |
| 43 | 29.6 | 4.3 | 2900  | US-07-918-314-5   | Sequence 5, Appli  |
| 44 | 29.4 | 4.2 | 3955  | US-09-214-278-4   | Sequence 4, Appli  |
| 45 | 29.2 | 4.2 | 16442 | US-08-781-891-208 | Sequence 208, App  |

## ALIGNMENTS

RESULT 1  
US-09-286-529-8  
; Sequence 8, Application US/09286529  
; Patent No. 6257367  
; GENERAL INFORMATION:  
; APPLICANT: Catherine Tribouley  
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
; FILE REFERENCE: 1408.003/200130.439C1  
; CURRENT APPLICATION NUMBER: US/09286,529  
; CURRENT FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 893  
; TYPE: DNA  
; ORGANISM: human  
US-09-286-529-8

Query Match 21.8%; Score 151.2; DB 4; Length 893;  
Best Local Similarity 57.9%; Pred. No. 3.6e-37;  
Matches 287; Conservative 0; Mismatches 208; Indels 1; Gaps 1;

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| QY | 4   | GATTGCCAAGAAATGACTGGACCAATGGGAGGCTGTCTCCTGCCAACGGTGT      | 63  | Sequence 8, Appli  |
| DB | 151 | GATTGCAGCAGCAGAGGAAATTCAGATCGATCGAAGCTGTCTCTGCAACAGTGC    | 210 | Sequence 16, Appli |
| QY | 64  | GGTCTTGACAGAGGATATCCAAAGATTGTGTATGAGAGGGTGGAGATGCTACTGC   | 123 | Sequence 1, Appli  |
| DB | 211 | GGACCTGGATGAGATTGTCAGAGAAATGTGCTTCATGAGGAGGATGACACATGT    | 270 | Sequence 1, Appli  |
| QY | 124 | ACAGCTGCTCTCTCTGCGATGACAAAGCAGCTGGGGCCACCAAAATGTAGATGTC   | 183 | Sequence 1, Appli  |
| DB | 271 | GGCCCTGAGGCGCGACCGGTTCAGAGAAAGATGCGGTTTCCAGAGTGAAGCATGT   | 330 | Sequence 3, Appli  |
| QY | 184 | ATCACCCTGTCTGTCATCATCTGTTGAGAGTCAATGACAGCTACTCTATGCT      | 243 | Sequence 7, Appli  |
| DB | 331 | GGGACTGTGCGCTGCTGTAACCGCTTTCAGAGGCGCACTGTCACACACAGTATGT   | 390 | Sequence 1, Appli  |
| QY | 244 | GTCTGTGGGAGACTTTTGGCCAGGTTTCTACCAAGACACGATTTGGAGGCTGCAGAC | 303 | Sequence 1, Appli  |
| DB | 391 | GTCTGTGGGAGACTGTCTGCGAGATTTTACCGAAGACCAAACTGTTGTTTCAAGAC  | 450 | Sequence 2, Appli  |
| QY | 304 | CAAGATGATCCCTGCGACGAGCAGACCCACCTGTGAGGTTCATGTGCTTCAG      | 363 | Sequence 10, Appli |
| DB | 451 | ATGAGATGTGTCTCTGCGAGAACCCACCTCTCTTACGACCACTGTACCGACAG     | 510 | Sequence 9, Appli  |
| QY | 364 | TTGACCTTAGTGGAGGAGATCCACACAGTGGCCCTCAGAGGCGCACTTTTGGC     | 423 | Sequence 1, Appli  |
| DB | 511 | GTGACCTTAGTGAAGATGCTCTCCACCGTCTCCACCGCTGCGGACGCGGTGCTGC   | 570 | Sequence 4, Appli  |



```

1  APPLICANT: West, James
2  APPLICANT: Tompkins, Christopher
3  TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID
4  NUMBER OF SEQUENCES: 18
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Cell Therapeutics, Inc.
7  STREET: 201 Elliott Avenue West
8  CITY: Seattle
9  STATE: Washington
10 COUNTRY: U.S.A.
11 ZIP: 98119
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: 3.5" disk, 1.44Mb, double side, high density
14 COMPUTER: PC Clone (486 microprocessor)
15 OPERATING SYSTEM: MS-DOS Version 6.1, Windows
16 SOFTWARE: WORD 6.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/09/400,742
19 FILING DATE:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 08/618,651
22 FILING DATE:
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Faciszewski, Stephen
25 REGISTRATION NUMBER: 36,131
26 REFERENCE/DOCKET NUMBER: 1801
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (206)282-7100
29 TELEFAX: (206)284-6206
30 INFORMATION FOR SEQ ID NO: 1:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 2242
33 TYPE: nucleic acid
34 STRANDEDNESS: double stranded
35 TOPOLOGY: linear
36 MOLECULE TYPE: cdna to mRNA
37 HYPOTHEICAL: no
38 ANTI-SENSE: no
39 FRAGMENT TYPE:
40 ORIGINAL SOURCE:
41 ORGANISM: homo sapien
42 STRAIN:
43 INDIVIDUAL ISOLATE:
44 DEVELOPMENTAL STAGE:
45 HAPLOTYPE:
46 TISSUE TYPE: brain
47 CELL TYPE:
48 ORGANELLE:
49 FEATURE:
50 NAME/KEY: hLPAATA
51 US-09-400-742-1
52
53 Query Match 4.6%; Score 32; DB 3; Length 2242;
54 Best Local Similarity 56.7%; Pred. No. 3.4;
55 Matches 59; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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57 QY 424 CTGCTGAGCACCCTGCTGATGGTGTATACCGCTTCGCGGGCTCTTCTCCCTAC 483
58 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
59 Db 352 CTGCTGCTCTTCCTGCTGCTCTCTCTCTCTGCTGCCACCTGTGGTCTGACGCCCA 411
60 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 QY 484 TGCAGCAGTTCTTCAACAGACATTTGCCAGCGGTGGAGGTTTGGT 527
62 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
63 Db 412 GCCAAGTACTTCTTCAAGATGGCCTTCAACATGGCTGGATGCT 455
64 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
65
66 RESULT 6
67 US-08-618-651A-1
68 ; Sequence 1, Application US/08618651A
69 ; Patent No. 6136964
70 ; GENERAL INFORMATION:
71 APPLICANT: Leung, David W.
72 APPLICANT: West, James

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APPLICANT: Tompkins, Christopher
TITLE OF INVENTION: MAMMALIAN LYOPHOSPHATIDIC ACID
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cell Therapeutics, Inc.
STREET: 201 Elliott Avenue West
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98119
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density
COMPUTER: PC Clone (486 microprocessor)
OPERATING SYSTEM: MS-DOS Version 6.1, Windows
SOFTWARE: WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618, 651A
FILING DATE: 15-Dec-1995
ATTORNEY/AGENT INFORMATION:
NAME: Faciszewski, Stephen
REGISTRATION NUMBER: 36,131
REFERENCE/DOCKET NUMBER: 1801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 282-7100
TELEFAX: (206) 284-6206
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2242
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: brain
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: hLpAATA
US-08-618-651A-1

Query Match 4.6%; Score 32; DB 3; Length 2242;
Best Local Similarity 56.7%; Pred. No. 3.4;
Matches 59; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 424 CTGCTGAGACACCGCTGCTAGTGTGTTTACCGCTGCGCTTCCTGCGCTCTTCTCTAC 483
DB 352 CTGCTGCTCTTCCTGCTGCTGCTCTCTCTCCCTGCGCCACCTGTGTGTTCTGACGCCCA 411
QY 484 TGCAGCAGTCTTCAACAGACATTCGCCAGCGGTGAGGTTGCT 527
DB 412 GCCAAGTACTTCTTCACAGATGCGCTTTCACATGCGTGATCT 455

RESULT 7
US-09-215-252-1
; Sequence 1, Application US/09215252
; Patent No. 6300487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADOUREL, Daniel
; APPLICANT: HOLLENBACK, David
; TITLE OF INVENTION: MAMMALIAN LYOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/215, 252

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INFORMATION FOR SEQ ID NO: 1  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3066 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHEetical: NO  
 ORIGINAL SOURCE:





APPLICATION NUMBER: US/08/705,557

```

FILING DATE: US/08/057,531
APPLICATION NUMBER: 07/833,431
FILING DATE: February 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: 96700/238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5595
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 52297
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: phage genome sequence
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: not applicable.
ORIGINAL SOURCE:
ORGANISM: mycobacteriophage L5
STRAIN: not applicable
INDIVIDUAL ISOLATE: L5
DEVELOPMENTAL STAGE: not applicable
HAPLOTYPE: not applicable
TISSUE TYPE: not applicable
CELL TYPE: not applicable
CELL LINE: not applicable
ORGANELLE: not applicable
IMMEDIATE SOURCE: mycobacteriophage L5 particles
POSITION IN GENOME: entire genome
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Hatfull and Sarkis
TITLE: DNA Sequence, Structure and Gene
Expression of Mycobacteriophage L5:
TITLE: A Phage System for Mycobacterial
Genetics
JOURNAL: Molecular Microbiology
VOLUME: 7
PAGES: 395-405
DATE: 1993
US-09-426-436-1

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[illegible]

Search completed: October 27, 2002, 02:42:37  
Job time : 154 secs